Phylogenetic Analysis and Polyphasic Characterization of Clavibacter michiganensis Strains Isolated from Tomato Seeds Reveal that Nonpathogenic Strains Are Distinct from C. michiganensis subsp. michiganensis

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Résumé en anglais	The genus Clavibacter comprises one species and five subspecies of plant-pathogenic bacteria, four of which are classified as quarantine organisms due to the high economic threat they pose. Clavibacter michiganensis subsp. michiganensis is one of the most important pathogens of tomato, but the recommended diagnostic tools are not satisfactory due to false-negative and/or -positive results. To provide a robust analysis of the genetic relatedness among a worldwide collection of C. michiganensis subsp. michiganensis strains, relatives (strains from the four other C. michiganensis subspecies), and nonpathogenic Clavibacter-like strains isolated from tomato, we performed multilocus sequence-based analysis and typing (MLSA and MLST) based on six housekeeping genes (atpD, dnaK, gyrB, ppK, recA, and rpoB). We compared this “framework” with phenotypic and genotypic characteristics such as pathogenicity on tomato, reaction to two antisera by immunofluorescence and to five PCR identification tests, and the presence of four genes encoding the main C. michiganensis subsp. michiganensis pathogenicity determinants. We showed that C. michiganensis subsp. michiganensis is monophyletic and is distinct from its closest taxonomic neighbors. The nonpathogenic Clavibacter-like strains were identified as C. michiganensis using 16S rRNA gene sequencing. These strains, while cross-reacting with C. michiganensis subsp. michiganensis identification tools, are phylogenetically distinct from the pathogenic strains but belong to the C. michiganensis clade. C. michiganensis subsp. michiganensis clonal complexes linked strains from highly diverse geographical origins and also strains isolated over long periods of time in the same location. This illustrates the importance of seed transmission in the worldwide dispersion of this pathogen and its survival and adaptation abilities in a new environment once introduced.
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